likely to act as a transcriptional modulator. HAP3 is divided into three domains, an amino terminal A domain, a central B domain, and a carboxyl terminal C domain, as shown diagrammatically in Figure 1A. Specifically, LEC1, has between about 75% and 85% sequence similarity, which is equivalent to 55% to 63% sequence identity, with the B domains of the other HAP3 homologs shown in Figure 1B; see also, Example 1, below. Figure 1B shows the amino acid sequence homology between LEC1 and other CBF homologs.--

Please replace the paragraph beginning on page 18, line 17, with the following rewritten paragraph.

--The nucleotide sequence for LEC1 corresponding to each domain is displayed in SEQ ID NO:1, *e.g.*, the A domain is located between about nucleotide position 1 to about nucleotide position 81; the B domain is located between about nucleotide position 82 to about nucleotide position 351; the C domain is located between about nucleotide position 352 to about nucleotide position 624.--

Please replace the paragraph beginning on page 18, line 25, with the following rewritten paragraph.

--The DNA binding activity, and, therefore, transcription activation function, of LEC1 polypeptides is thought to be modulated by a short region of seven residues, MPIANVI (SEQ ID NO:5) (found, *e.g.*, at residues 34-40 of SEQ ID NO:2). Thus, the polypeptides of the invention will often retain these sequences.--

Please delete the paragraph beginning on page 23, line 3.

Please replace the paragraph beginning on page 31, line 22, with the following rewritten paragraph.

--The genomic library of lec1-2 was screened using right and left T-DNA specific probes according to standard techniques. About 12 clones that cosegregate with the mutation, were isolated and purified and the entire DNAs were further labeled and used as probes to screen a southern blot containing wild type and lec1-1 genomic DNA. One clone hybridized with plant